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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/023,584

DATE: 05/03/2002

TIME: 14:31:58

Input Set : N:\Crf3\RULE60\10023584.raw

Output Set: N:\CRF3\05032002\J023584.raw

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MAY 15 2002

TECH CENTER 1600/2900

1 <110> APPLICANT: Rosen et al.
 2 <120> TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
 3 <130> FILE REFERENCE: PF112P1
 4 <140> CURRENT APPLICATION NUMBER: 10/023,584
 C--> 5 <141> CURRENT FILING DATE: 2001-12-21
 7 <150> PRIOR APPLICATION NUMBER: 08/465,968
 8 <151> PRIOR FILING DATE: 1995-06-06
 11 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/207,550
 W--> 12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1994-03-08
 13 <160> NUMBER OF SEQ ID NOS: 10
 14 <170> SOFTWARE: PatentIn Ver. 2.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1674
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
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 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (12)..(1268)
 23 <220> FEATURE:
 24 <221> NAME/KEY: sig_peptide
 25 <222> LOCATION: (12)..(149)
 26 <220> FEATURE:
 27 <221> NAME/KEY: mat_peptide
 28 <222> LOCATION: (150)..(1268)
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 31 Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu
 32 -45 -40 -35
 33 ctc gcc gct gcg ctg ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc 98
 34 Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala
 35 -30 -25 -20
 36 gcc gcc ttc gag tcc gga ctc gac ctc tcg gac gcg gag ccc gac gcg 146
 37 Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
 38 -15 -10 -5
 39 ggc gag gcc acg gct tat gca agc aaa gat ctg gag gag cag tta cgg 194
 40 Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg
 41 -1 1 5 10 15
 42 tct gtg tcc agt gta gat gaa ctc atg act gta ctc tac cca gaa tat 242
 43 Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr
 44 20 25 30
 45 tgg aaa atg tac aag tgt cag cta agg aaa gga ggc tgg caa cat aac 290
 46 Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn
 47 35 40 45

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48	aga gaa cag gcc aac ctc aac tca agg aca gaa gag act ata aaa ttt	338
49	Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe	
50	50 55 60	
51	gct gca gca cat tat aat aca gag atc ttg aaa agt att gat aat gag	386
52	Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu	
53	65 70 75	
54	tgg aga aag act caa tgc atg cca cgg gag gtg tgt ata gat gtg ggg	434
55	Trp Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly	
56	80 85 90 95	
57	aag gag ttt gga gtc gcg aca aac acc ttc ttt aaa cct cca tgt gtg	482
58	Lys Glu Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val	
59	100 105 110	
60	tcc gtc tac aga tgt ggg ggt tgc tgc aat agt gag ggg ctg cag tgc	530
61	Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys	
62	115 120 125	
63	atg aac acc agc acg agc tac ctc agc aag acg tta ttt gaa att aca	578
64	Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr	
65	130 135 140	
66	gtg cct ctc tct caa ggc ccc aaa cca gta aca atc agt ttt gcc aat	626
67	Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn	
68	145 150 155	
69	cac act tcc tgc cga tgc atg tct aaa ctg gat gtt tac aga caa gtt	674
70	His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val	
71	160 165 170 175	
72	cat tcc att att aga cgt tcc ctg cca gca aca cta cca cag tgt cag	722
73	His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln	
74	180 185 190	
75	gca gcg aac aag acc tgc ccc acc aat tac atg tgg aat aat cac atc	770
76	Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile	
77	195 200 205	
78	tgc aga tgc ctg gct cag gaa gat ttt atg ttt tcc tcg gat gct gga	818
79	Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly	
80	210 215 220	
81	gat gac tca aca gat gga ttc cat gac atc tgt gga cca aac aag gag	866
82	Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu	
83	225 230 235	
84	ctg gat gaa gag acc tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct	914
85	Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro	
86	240 245 250 255	
87	gcc agc tgt gga ccc cac aaa gaa cta gac aga aac tca tgc cag tgt	962
88	Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys	
89	260 265 270	
90	gtc tgt aaa aac aaa ctc ttc ccc agc caa tgt ggg gcc aac cga gaa	1010
91	Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu	
92	275 280 285	
93	ttt gat gaa aac aca tgc cag tgt gta tgt aaa aga acc tgc ccc aga	1058
94	Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg	
95	290 295 300	
96	aat caa ccc cta aat cct gga aaa tgt gcc tgt gaa tgt aca gaa agt	1106

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97      Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser
98      305                      310                      315
99      cca cag aaa tgc ttg tta aaa gga aag aag ttc cac cac caa aca tgc 1154
100     Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys
101     320                      325                      330                      335
102     agc tgt tac aga cgg cca tgt acg aac cgc cag aag gct tgt gag cca 1202
103     Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro
104     340                      345                      350
105     gga ttt tca tat agt gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg 1250
106     Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp
107     355                      360                      365
108     caa aga cca caa atg agc taagattgta ctgtttttcca gttcatcgat 1298
109     Gln Arg Pro Gln Met Ser
110     370
111     tttctattat ggaaaaactgt gttgccacag tagaactgtc tgtgaacaga gagacccttg 1358
112     tgggtccatg ctaacaaaga caaaagtctg tcttttcctga accatgtgga taactttaca 1418
113     gaaatggact ggagctcatc tgcaaaaggc ctcttgtaaa gactggtttt ctgccaatga 1478
114     ccaaacagcc aagatttttcc tcttggtgatt tctttaaaag aatgactata taattttatt 1538
115     ccactaaaaa tattgttttct gcattcattt ttatagcaac aacaattggg aaaactcact 1598
116     gtgatcaata tttttatatc atgcaaaaata tgtttaaaat aaaatgaaaa ttgtatttat 1658
117     aaaaaaaaaa aaaaaa 1674
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 419
121 <212> TYPE: PRT
122 <213> ORGANISM: Homo sapiens
123 <400> SEQUENCE: 2
124     Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
125     -45                      -40                      -35
126     Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
127     -30                      -25                      -20                      -15
128     Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
129     -10                      -5                      -1 1
130     Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
131     5                      10                      15
132     Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
133     20                      25                      30
134     Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
135     35                      40                      45                      50
136     Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
137     55                      60                      65
138     His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
139     70                      75                      80
140     Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
141     85                      90                      95
142     Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
143     100                      105                      110
144     Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
145     115                      120                      125                      130
146     Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu

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147                               135                               140                               145
148 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
149                               150                               155                               160
150 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
151                               165                               170                               175
152 Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
153                               180                               185                               190
154 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
155                               195                               200                               205                               210
156 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
157                               215                               220                               225
158 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
159                               230                               235                               240
160 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
161                               245                               250                               255
162 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
163                               260                               265                               270
164 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
165                               275                               280                               285                               290
166 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
167                               295                               300                               305
168 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
169                               310                               315                               320
170 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
171                               325                               330                               335
172 Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
173                               340                               345                               350
174 Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro
175                               355                               360                               365                               370
176 Gln Met Ser
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 196
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
182 <400> SEQUENCE: 3
183 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
184 1 5 10 15
185 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
186 20 25 30
187 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
188 35 40 45
189 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
190 50 55 60
191 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
192 65 70 75 80
193 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
194 85 90 95
195 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
196 100 105 110

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197   Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
198           115                      120                      125
199   Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
200           130                      135                      140
201   Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
202   145                      150                      155                      160
203   Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
204           165                      170                      175
205   Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
206           180                      185                      190
207   Thr Asp Val Arg
208           195
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 241
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 4
215   Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
216       1              5              10              15
217   Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
218           20              25              30
219   Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
220           35              40              45
221   His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
222       50              55              60
223   Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
224       65              70              75              80
225   Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
226           85              90              95
227   Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
228           100             105             110
229   Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
230           115             120             125
231   Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
232       130             135             140
233   Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
234       145             150             155             160
235   Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
236           165             170             175
237   Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
238           180             185             190
239   Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
240           195             200             205
241   Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
242       210             215             220
243   Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
244       225             230             235             240
245   Ala
247 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/023,584

DATE: 05/03/2002
TIME: 14:31:59

Input Set : N:\Crf3\RULE60\10023584.raw
Output Set: N:\CRF3\05032002\J023584.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 2,5,6,7,10

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/023,584

DATE: 05/03/2002
TIME: 14:31:59

Input Set : N:\Crf3\RULE60\10023584.raw
Output Set: N:\CRF3\05032002\J023584.raw

Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:6; Xaa Pos. 2,5,6,7,10

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/023,584

DATE: 05/03/2002

TIME: 14:31:59

Input Set : N:\Crf3\RULE60\10023584.raw

Output Set: N:\CRF3\05032002\J023584.raw

L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:288 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6